

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/521,401A

Source: PGF

Date Processed by STIC: 12/8/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 12/08/2005

PATENT APPLICATION: US/10/521,401A

TIME: 08:22:39

Input Set : E:\MSQ01-003-US Corrected SEQUENCE LISTING.txt

Output Set: N:\CRF4\12082005\J521401A.raw

```

2 <110> APPLICANT: Health Protection Agency
3     Sutton, John
4     Shone, Clifford
W--> 5 <120> TITLE OF INVENTION: Targeted Agents for Nerve Regeneration
W--> 6 <130> FILE REFERENCE: GWS/CMS/24346WO
C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/521,401A
C--> 7 <141> CURRENT FILING DATE: 2005-01-18
8 <150> PRIOR APPLICATION NUMBER: GB 0216865.6
8 <151> PRIOR FILING DATE: 2002-07-19
W--> 9 <160> NUMBER OF SEQ ID: 24
10 <170> SOFTWARE: PatentIn version 3.1
W--> 11 <210> SEQ ID NO: 1
12 <211> LENGTH: 215
13 <212> TYPE: PRT
14 <213> ORGANISM: Artificial Sequence
W--> 15 <220> FEATURE:
16 <223> OTHER INFORMATION: Synthetic
18 <400> SEQUENCE: 1
20 Ile Glu Gly Arg Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile
21 1 5 10 15
24 Asp Gln Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu
25 20 25 30
28 Ser Lys Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser
29 35 40 45
32 Glu Ile Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe
33 50 55 60
36 Pro Ser Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn
37 65 70 75 80
40 Lys Met Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro
41 85 90 95
44 Ala Tyr Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly
45 100 105 110
48 Thr Ile Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn
49 115 120 125
52 Lys Asp Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val
53 130 135 140
56 Ser Gln Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys
57 145 150 155 160
60 Gly Ser Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln
61 165 170 175
64 Leu Glu Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met
65 180 185 190
68 Arg Leu Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met

```

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```

69          195          200          205
72 Gly Thr Ala Ile Asn Pro Lys
73      210          215
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 212
78 <212> TYPE: PRT
79 <213> ORGANISM: Artificial Sequence
W--> 80 <220> FEATURE:
81 <223> OTHER INFORMATION: Synthetic
83 <400> SEQUENCE: 2
85 Ala Glu Thr Lys Asn Phe Thr Asp Leu Val Glu Ala Thr Lys Trp Gly
86 1          5          10          15
89 Asn Ser Leu Ile Lys Ser Ala Lys Tyr Ser Ser Lys Asp Lys Met Ala
90      20          25          30
93 Ile Tyr Asn Tyr Thr Lys Asn Ser Ser Pro Ile Asn Thr Pro Leu Arg
94      35          40          45
97 Ser Ala Asn Gly Asp Val Asn Lys Leu Ser Glu Asn Ile Gln Glu Gln
98      50          55          60
101 Val Arg Gln Leu Asp Ser Thr Ile Ser Lys Ser Val Thr Pro Asp Ser
102 65          70          75          80
105 Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Ser Ser Ile Thr
106      85          90          95
109 Gly Phe Thr Arg Glu Asp Leu His Met Leu Gln Gln Thr Asn Asn Gly
110      100          105          110
113 Gln Tyr Asn Glu Ala Leu Val Ser Lys Leu Asn Asn Leu Met Asn Ser
114      115          120          125
117 Arg Ile Tyr Arg Glu Asn Gly Tyr Ser Ser Thr Gln Leu Val Ser Gly
118      130          135          140
121 Ala Ala Leu Ala Gly Arg Pro Ile Glu Leu Lys Leu Glu Leu Pro Lys
122 145          150          155          160
125 Gly Thr Lys Ala Ala Tyr Ile Asp Ser Lys Glu Leu Thr Ala Tyr Pro
126      165          170          175
129 Gly Gln Gln Glu Val Leu Leu Pro Arg Gly Thr Glu Tyr Ala Val Gly
130      180          185          190
133 Ser Val Lys Leu Ser Asp Asn Lys Arg Lys Ile Ile Ile Thr Ala Val
134      195          200          205
137 Val Phe Lys Lys
138      210
141 <210> SEQ ID NO: 3
142 <211> LENGTH: 636
143 <212> TYPE: PRT
144 <213> ORGANISM: Artificial Sequence
W--> 145 <220> FEATURE:
146 <223> OTHER INFORMATION: Synthetic
148 <400> SEQUENCE: 3
150 Gly Cys Thr Gly Ala Ala Ala Cys Cys Ala Ala Ala Ala Ala Cys Thr
151 1          5          10          15
154 Thr Cys Ala Cys Cys Gly Ala Cys Cys Thr Gly Gly Thr Thr Gly Ala
155      20          25          30

```

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```

158 Ala Gly Cys Thr Ala Cys Cys Ala Ala Ala Thr Gly Gly Gly Gly Thr
159      35      40      45
162 Ala Ala Cys Thr Cys Thr Cys Thr Gly Ala Thr Cys Ala Ala Ala Thr
163      50      55      60
166 Cys Thr Gly Cys Thr Ala Ala Ala Thr Ala Cys Thr Cys Thr Thr Cys
167 65      70      75      80
170 Thr Ala Ala Ala Gly Ala Cys Ala Ala Ala Ala Thr Gly Gly Cys Thr
171      85      90      95
174 Ala Thr Cys Thr Ala Cys Ala Ala Cys Thr Ala Cys Ala Cys Cys Ala
175      100     105     110
178 Ala Ala Ala Ala Cys Thr Cys Thr Thr Cys Thr Cys Cys Gly Ala Thr
179      115     120     125
182 Cys Ala Ala Cys Ala Cys Cys Cys Gly Cys Thr Gly Cys Gly Thr
183      130     135     140
186 Thr Cys Thr Gly Cys Thr Ala Ala Cys Gly Gly Thr Gly Ala Cys Gly
187 145     150     155     160
190 Thr Thr Ala Ala Cys Ala Ala Ala Cys Thr Gly Thr Cys Thr Gly Ala
191      165     170     175
194 Ala Ala Ala Cys Ala Thr Cys Cys Ala Gly Gly Ala Ala Cys Ala Gly
195      180     185     190
198 Gly Thr Thr Cys Gly Thr Cys Ala Gly Cys Thr Gly Gly Ala Cys Thr
199      195     200     205
202 Cys Thr Ala Cys Cys Ala Thr Cys Thr Cys Thr Ala Ala Ala Thr Cys
203      210     215     220
206 Thr Gly Thr Thr Ala Cys Cys Cys Cys Gly Gly Ala Cys Thr Cys Thr
207 225     230     235     240
210 Gly Thr Thr Thr Ala Cys Gly Thr Thr Thr Ala Cys Cys Gly Thr Cys
211      245     250     255
214 Thr Gly Cys Thr Gly Ala Ala Cys Cys Thr Gly Gly Ala Cys Thr Ala
215      260     265     270
218 Cys Cys Thr Gly Thr Cys Thr Thr Cys Thr Ala Thr Cys Ala Cys Cys
219      275     280     285
222 Gly Gly Thr Thr Thr Cys Ala Cys Cys Cys Gly Thr Gly Ala Ala Gly
223      290     295     300
226 Ala Cys Cys Thr Gly Cys Ala Cys Ala Thr Gly Cys Thr Gly Cys Ala
227 305     310     315     320
230 Gly Cys Ala Gly Ala Cys Cys Ala Ala Cys Ala Ala Cys Gly Gly Thr
231      325     330     335
234 Cys Ala Gly Thr Ala Cys Ala Ala Cys Gly Ala Ala Gly Cys Thr Cys
235      340     345     350
238 Thr Gly Gly Thr Thr Thr Cys Thr Ala Ala Ala Cys Thr Gly Ala Ala
239      355     360     365
242 Cys Ala Ala Cys Cys Thr Gly Ala Thr Gly Ala Ala Cys Thr Cys Thr
243      370     375     380
246 Cys Gly Thr Ala Thr Cys Thr Ala Cys Cys Gly Thr Gly Ala Ala Ala
247 385     390     395     400
250 Ala Cys Gly Gly Thr Thr Ala Cys Thr Cys Thr Thr Cys Thr Ala Cys
251      405     410     415
254 Cys Cys Ala Gly Cys Thr Gly Gly Thr Thr Thr Cys Thr Gly Gly Thr

```

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```

255          420          425          430
258 Gly Cys Thr Gly Cys Thr Cys Thr Gly Gly Cys Thr Gly Gly Thr Cys
259          435          440          445
262 Gly Thr Cys Cys Gly Ala Thr Cys Gly Ala Ala Cys Thr Gly Ala Ala
263          450          455          460
266 Ala Cys Thr Gly Gly Ala Ala Cys Thr Gly Cys Cys Gly Ala Ala Ala
267 465          470          475          480
270 Gly Gly Thr Ala Cys Cys Ala Ala Ala Gly Cys Thr Gly Cys Thr Thr
271          485          490          495
274 Ala Cys Ala Thr Cys Gly Ala Cys Thr Cys Thr Ala Ala Ala Gly Ala
275          500          505          510
278 Ala Cys Thr Gly Ala Cys Cys Gly Cys Thr Thr Ala Cys Cys Cys Cys
279          515          520          525
282 Gly Gly Thr Cys Ala Gly Cys Ala Gly Gly Ala Ala Gly Thr Thr Cys
283          530          535          540
286 Thr Gly Cys Thr Gly Cys Cys Gly Cys Gly Thr Gly Gly Thr Ala Cys
287 545          550          555          560
290 Cys Gly Ala Ala Thr Ala Cys Gly Cys Thr Gly Thr Thr Gly Gly Thr
291          565          570          575
294 Thr Cys Thr Gly Thr Thr Ala Ala Ala Cys Thr Gly Thr Cys Thr Gly
295          580          585          590
298 Ala Cys Ala Ala Cys Ala Ala Ala Cys Gly Thr Ala Ala Ala Ala Thr
299          595          600          605
302 Cys Ala Thr Cys Ala Thr Cys Ala Cys Cys Gly Cys Thr Gly Thr Thr
303          610          615          620
306 Gly Thr Thr Thr Thr Cys Ala Ala Gly Ala Ala Gly
307 625          630          635
310 <210> SEQ ID NO: 4
311 <211> LENGTH: 212
312 <212> TYPE: PRT
313 <213> ORGANISM: Staphylococcus aureus
W--> 314 <400> SEQUENCE: 4
316 Ala Asp Val Lys Asn Phe Thr Asp Leu Asp Glu Ala Thr Lys Trp Gly
317 1          5          10          15
320 Asn Lys Leu Ile Lys Gln Ala Lys Tyr Ser Ser Asp Asp Lys Ile Ala
321          20          25          30
324 Leu Tyr Glu Tyr Thr Lys Asp Ser Ser Lys Ile Asn Gly Pro Leu Arg
325          35          40          45
328 Leu Ala Gly Gly Asp Ile Asn Lys Leu Asp Ser Thr Thr Gln Asp Lys
329          50          55          60
332 Val Arg Arg Leu Asp Ser Ser Ile Ser Lys Ser Thr Thr Pro Glu Ser
333 65          70          75          80
336 Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Thr Ser Ile Val
337          85          90          95
340 Gly Phe Thr Asn Glu Asp Leu Tyr Lys Leu Gln Gln Thr Asn Asn Gly
341          100          105          110
344 Gln Tyr Asp Glu Asn Leu Val Arg Lys Leu Asn Asn Val Met Asn Ser
345          115          120          125
348 Arg Ile Tyr Arg Glu Asp Gly Tyr Ser Ser Thr Gln Leu Val Ser Gly

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Input Set : E:\MSQ01-003-US Corrected SEQUENCE LISTING.txt

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```

349      130      135      140
352 Ala Ala Val Gly Gly Arg Pro Ile Glu Leu Arg Leu Glu Leu Pro Lys
353 145      150      155      160
356 Gly Thr Lys Ala Ala Tyr Leu Asn Ser Lys Asp Leu Thr Ala Tyr Tyr
357      165      170      175
360 Gly Gln Gln Glu Val Leu Leu Pro Arg Gly Thr Glu Tyr Ala Val Gly
361      180      185      190
364 Ser Val Glu Leu Ser Asn Asp Lys Lys Lys Ile Ile Ile Thr Ala Ile
365      195      200      205
368 Val Phe Lys Lys
369      210
372 <210> SEQ ID NO: 5
373 <211> LENGTH: 247
374 <212> TYPE: PRT
375 <213> ORGANISM: Staphylococcus aureus
W--> 376 <400> SEQUENCE: 5
378 Met Lys Arg Lys Leu Phe Phe Lys Ile Ile Phe Val Leu Ser Leu Val
379 1      5      10      15
382 Leu Ser Ile His Ser Ile Asn Asp Arg Thr Thr Glu Leu Ser Asn Ile
383      20      25      30
386 Ala Leu Ala Asp Asp Val Lys Asn Phe Thr Asp Leu Thr Glu Ala Thr
387      35      40      45
390 Asn Trp Gly Asn Lys Leu Ile Lys Gln Ala Asn Tyr Ser Ser Lys Asp
391      50      55      60
394 Lys Glu Ala Ile Tyr Asn Tyr Thr Lys Tyr Ser Ser Pro Ile Asn Thr
395 65      70      75      80
398 Pro Leu Arg Ser Ser Gln Gly Asp Ile Ser Asn Phe Ser Ala Asp Leu
399      85      90      95
402 Gln Glu Lys Ile Leu Arg Leu Asp Arg Leu Ile Ser Lys Ser Ser Thr
403      100      105      110
406 Ser Asp Ser Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Ser
407      115      120      125
410 Ser Val Lys Gly Phe Ser Ser Glu Asp Leu Glu Leu Leu Tyr Lys Thr
411      130      135      140
414 Glu Asn Gly Lys Tyr Asn Glu Glu Leu Val Lys Lys Leu Asn Asn Ile
415 145      150      155      160
418 Met Asn Ser Lys Ile Tyr Thr Glu Tyr Gly Tyr Ser Ser Thr Gln Leu
419      165      170      175
422 Val Lys Gly Ala Ala Leu Ala Gly Arg Pro Ile Glu Leu Lys Leu Gln
423      180      185      190
426 Leu Pro Lys Gly Thr Lys Ala Ala Tyr Ile Asp Ser Lys Asn Leu Thr
427      195      200      205
430 Ala Tyr Pro Gly Gln Gln Glu Ile Leu Leu Pro Arg Gly Thr Asp Tyr
431      210      215      220
434 Thr Ile Asn Thr Val Lys Leu Ser Asp Asp His Lys Arg Ile Leu Ile
435 225      230      235      240
438 Glu Gly Ile Val Phe Lys Lys
439      245
442 <210> SEQ ID NO: 6

```

**VERIFICATION SUMMARY**

DATE: 12/08/2005

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TIME: 08:22:40

Input Set : E:\MSQ01-003-US Corrected SEQUENCE LISTING.txt

Output Set: N:\CRF4\12082005\J521401A.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier  
L:6 M:283 W: Missing Blank Line separator, <130> field identifier  
L:7 M:270 C: Current Application Number differs, Replaced Current Application No  
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:9 M:283 W: Missing Blank Line separator, <160> field identifier  
L:11 M:283 W: Missing Blank Line separator, <210> field identifier  
L:15 M:283 W: Missing Blank Line separator, <220> field identifier  
L:80 M:283 W: Missing Blank Line separator, <220> field identifier  
L:145 M:283 W: Missing Blank Line separator, <220> field identifier  
L:314 M:283 W: Missing Blank Line separator, <400> field identifier  
L:376 M:283 W: Missing Blank Line separator, <400> field identifier  
L:446 M:283 W: Missing Blank Line separator, <400> field identifier  
L:508 M:283 W: Missing Blank Line separator, <400> field identifier  
L:554 M:283 W: Missing Blank Line separator, <400> field identifier  
L:604 M:283 W: Missing Blank Line separator, <400> field identifier  
L:674 M:283 W: Missing Blank Line separator, <400> field identifier  
L:744 M:283 W: Missing Blank Line separator, <400> field identifier  
L:966 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1088 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1365 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1642 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1823 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1836 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1853 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1866 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1883 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1896 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1913 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1927 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1940 M:283 W: Missing Blank Line separator, <220> field identifier